

Table 1. Protein identification from SDS-PAGE bands by MALDI-TOF-MS.

Spot no.	Accession no.	Protein name	Species	Protein score ^a	Protein score C.I.%	Total Ion score	Total ion score CI%	Number of matching peptides	Sequence coverage %	Protein PI	Protein MW (kDa)
1	gi 298543883	starch synthase II	<i>Triticum aestivum</i>	143	100	106	100	10	12.5	6.27	87.139
2	gi 58618129	starch branching enzyme IIb	<i>Triticum aestivum</i>	166	100	141	100	9	11.1	5.75	94.629
3	gi 399153332	waxy protein	<i>Triticum aestivum</i>	649	100	468	100	22	36.7	7.85	67.165
4	gi 452113211	waxy protein	<i>Aegilops</i>	518	100	401	100	16	26.5	7.85	67.100
5	gi 357110669	granule-bound starch synthase 1	<i>Brachypodium distachyon</i>	128	100	86	99.9	15	25	7.12	66.219

a: Protein Score: statistical probability of true positive identification of the predicted protein calculated by MASCOT (score $\geq$ 42 against NCBIInr).